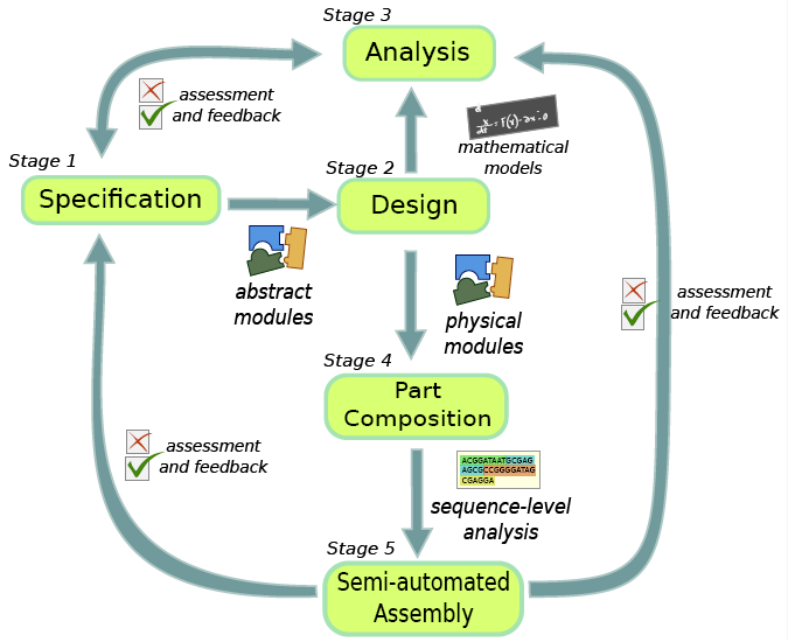
Herbert Sauro

University of Washington

Emerging Standards in Synthetic Biology

Herbert M Sauro
Michal Galdzicki and Deepak Chandran
University of Washington, Seattle
And the Synthetic Biology Data Exchange Working Group

Overall Aim of the Standardization Effort



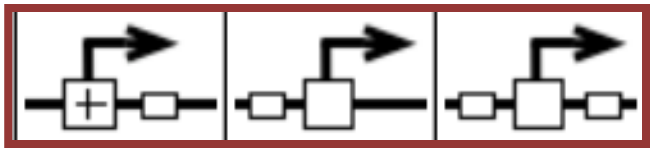
Specifically:

- To allow researches to electronically exchange designs with round-tripping.
- To send designs to bio-fabrication centers for assembly.
- To allow storage of designs in repositories and for publication purposes.

Synthetic Biology Data Exchange Group

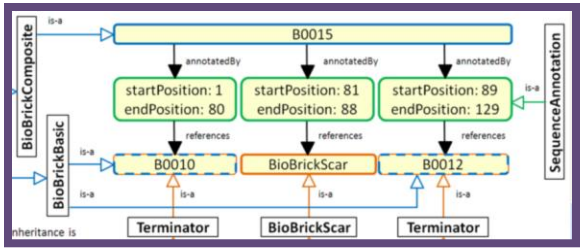
Synthetic Biology Open Language (SBOL)

http://www.sbolstandard.org/



SBOL-visual

biofab



SBOL-semantic

UNIVERSITY of WASHINGTON

Clotho

BOSTON UNIVERSITY

Berkeley UNIVERSITY OF CALIFORNIA

TinkerCell

UNIVERSITY of WASHINGTON

GenoCAD

VIRGINIA BIOINFORMATICS INSTITUTE AT VIRGINIA TECH

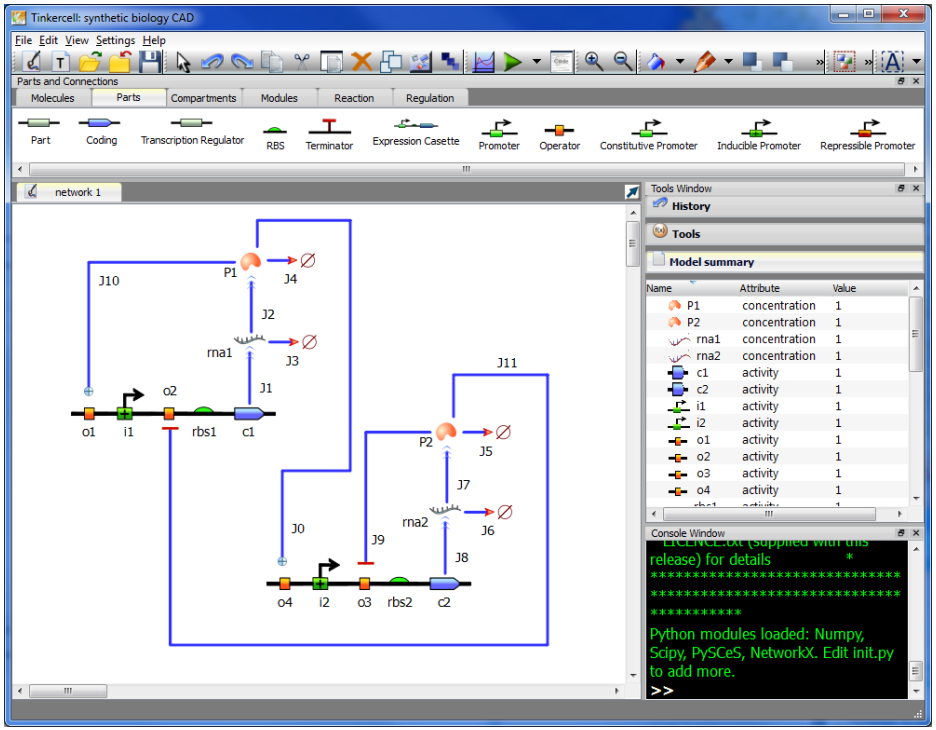
jbeir public

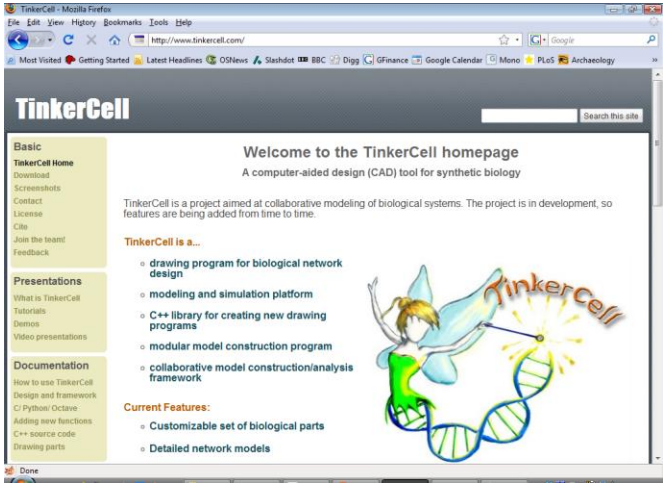
jbei Joint BioEnergy Institute

iBioSim

THE UNIVERSITY OF UTAH

UW Efforts: A CAD system for Synthetic Biology called TinkerCell





www.tinkercell.com (Windows, Mac and Linux, released under BSD)

Contact author for details (dchandran1@gmail.com)

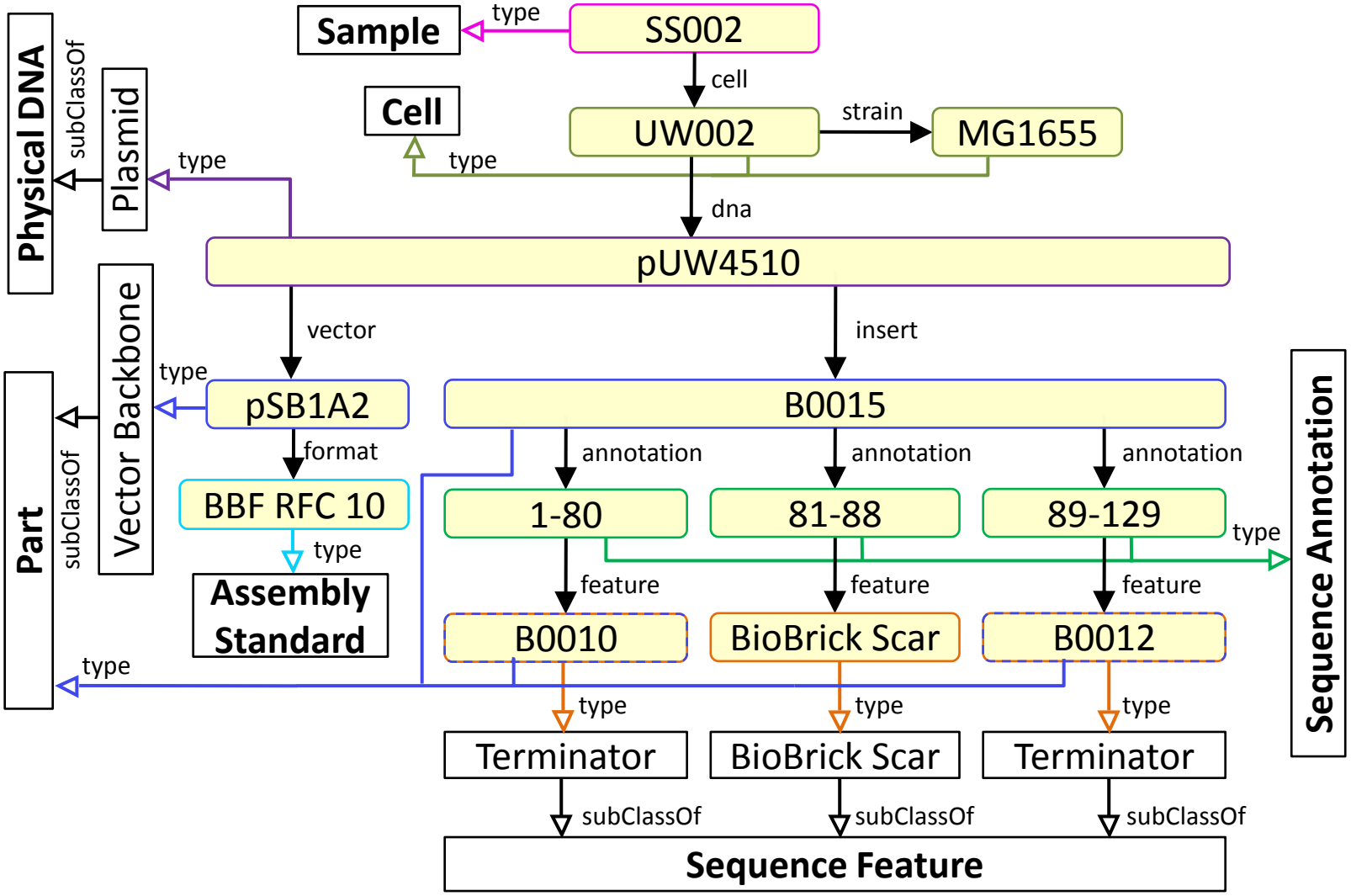


Figure 1. Diagram of the SBOL Semantic structure, illustrated with a set of information about a synthetic biology construct. **a.** A simplified *Class* (black rectangles) hierarchy (black open faced arrows) describes types (colored open faced arrows)of *Individual* data elements (yellow rounded rectangles) and the composition relationships between them (closed faced arrows). The example can be read as: Sample (pink) SS002 contains UW002 cells (dark green) of the MG1655 *E. coli* strain, which contain a plasmid (purple) pUW4510, which is composed of an parts (dark blue) an insert B0015 and vector backbone pSB1A2. The pSB1A2 vector backbone complies with the Assembly Standard (light blue) BBF RFC 10. The B0015 sequence annotations (green) specify three features (orange), the BioBrick Scar, and the parts (blue and orange indicating multiple inheritance), B0010 and B0012, which serve as transcriptional termination signals. **b.** Data type *Properties* used to hold information for each SBOL class follow the colon.

List of Software in the Working Group

- **Clotho (BU,Berkeley), Java**

  Connects users to repositories of biological parts. Plugin tools then define the various functions that can be performed, mainly related to lab and parts managements.

- **GenoCAD (VT)**

  Web based tool for the design of biological devices using an attribute grammar which defines the legal composition of parts.

- **iBioSim (Utah), Java**

  Advanced simulation and analysis tool for synthetic and systems biology

- **JBEI Repository (Java), DOE support infrastructure**

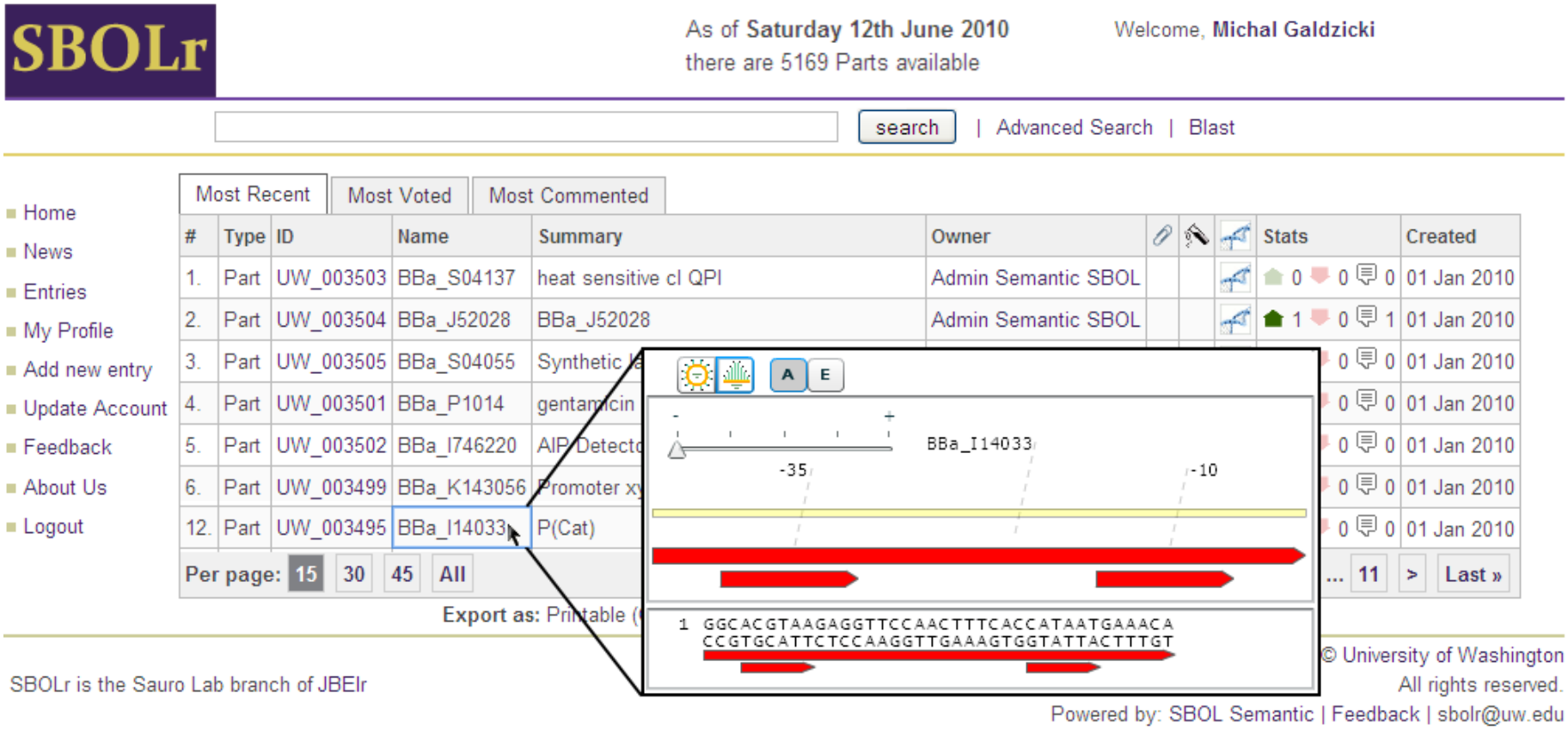
- **SBOLr (Currently Python but moving to Java)**

  Test parts repository, ~5000 parts

- **TinkerCell (UW), C++/Qt**

  Extensible visual design tool with support for modules, eg simulation, annotation.

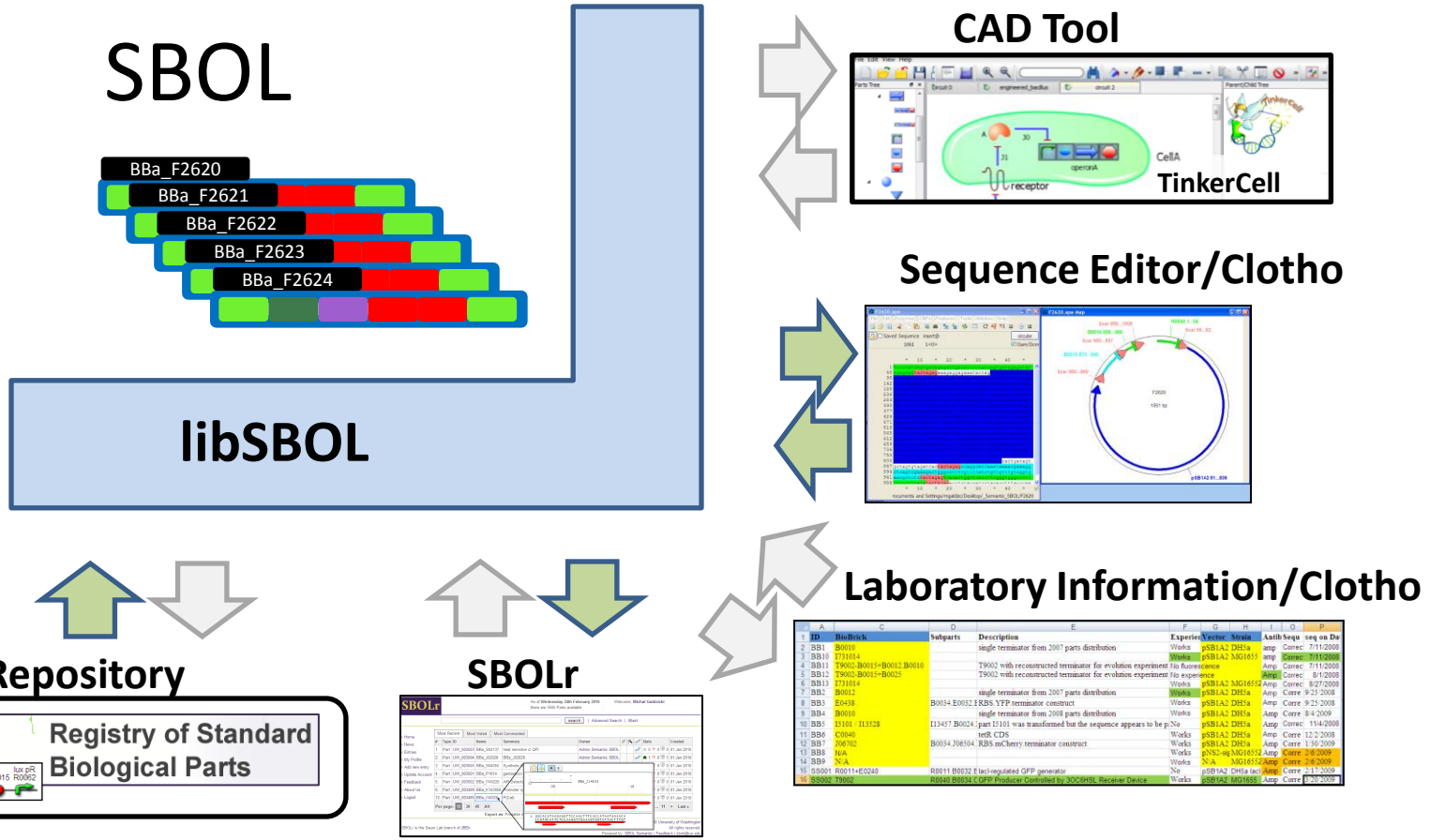
SBOLr is knowledge base of 5169 biological parts, used as a test database for the working group.



http://sbolr.bhi.washington.edu/

JBEIr Software by Timothy Ham & Zinovii Dmytriv

libSBOL: Supports SBOL format for other third-party tools



Acknowledgements: Collaborators and Funding

UW

Deepak Chandran, Michal Galdziki, Sean Sleight, Bryan Bartley, Alex Neilson

BioFAB (Berkeley, Stanford)

Cesar Rodriguez, Drew Endy , Chris Anderson

Utah

Chris Myers

Virginia Tech

Jean Peccoud

JBEI (DOE)

Timothy Ham & Zinovii Dmytriv

Boston University

Douglas Densmore

CRG, Spain

Raik Grunberg

Funding

National Library of Medicine (Galdziki)
Other funding scraped from NIH (JSIm/SBW) , NIH (SBW) and NSF (FIBR), Microsoft Strategic Research, BioFAB, JBEI